

FIGURE 1

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGA
GAGAAGCGCCTGCAGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAA
AGGCTCCACAAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCC
CAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGA
AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCT
CTGTGGAGGCAGAGCCAGTGGAGCCCAGTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCA
ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCGCTGACGGCCAGGGTGAAGCATG
TGAGGAGCCGCCCCGGAGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGA
ATAACCACCATTTTGAAGGACC**ATG**AGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG
CTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTTTGAGGGCACTGAGGAGGGCTC
GCCAAGAGAGTTTCATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGACAAGTGCA
CCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAG
CCTGAGGTGCTTCTGGAGAACCGAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCT
GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTG
TGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC
TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCAGCT
GGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC
TGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCACAACCAATCAGAGATCATCGCGCAG
CTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCAGCCACCCCCCGCTGC
CCCGCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACG
AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCTCTGCCCACTATGCCCACTCTC
ACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGGCCCATGGAGAGACTGCCTGCAGGCCCT
GGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTCA
TGCAGGTGTGGTGGGACAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTG
GATGGCTCTGTAACTTCTTCAGGAAGTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGA
CGGCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTGACGAACCAAGGCAACTACAAC
TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTCTTTGCAGAATACGCCAGTTTCCGC
CTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGGGTGA
CTCCTTTACATGGCACAACGGCAAGCAGTTCACCACCCTGGACAGAGATCATGATGTCTACA
CAGGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAAC
CTCAACGGGGTCTGGTACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTG
GGCTGAGTTCCGAGGAGGCTCTTACTCACTCAAGAAAGTGGTGATGATGATCCGACCGAACC
CCAACACCTTCCAC**TAA**GCCAGCTCCCCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCA
CCCTGGTCAAGCTGGCCACAGCACAAAGAACAACCTCCTCACCAGTTCATCCTGAGGCTGGGA
GGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAAGTGAATCGAT
ACGGTGTTTTCTGTCCCTCCTACTTTCTTACACCAGACAGCCCCCTCATGTCTCCAGGACA
GGACAGGACTACAGACAACCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAA

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FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
QRVGTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLR
KESRNMNSRVLTQLYMQLLHEIIRKRDNALELSQLENRIINQTDMLQLASKYKDLEHKYQHL
ATLAHNQSEIIAQLEEHQCRVPSARVPVQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSIYLVKPENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFFRNWETKQGGFGNIDGEYWLGLENIYWLTNQGNKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYHQ
KGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKKVMMIRPNPNTFH
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Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites.

amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,
465-471, 473-479

Amidation site.

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins.

amino acids 275-292

CCCACGCGTCCGGCGCCGTGGCCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT
GTTCCCTCTTTTCGGGGGTCTTCAACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAATTCC
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACCTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGTTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAA
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

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FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26846

<subunit 1 of 1, 117 aa, 1 stop

<MW: 12692, pI: 7.50, NX(S/T): 0

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ

AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDK

Important features:

Signal peptide:

amino acids 1-16

N-myristoylation sites.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAA
GCCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCGAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCACTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTCACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG
CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGMTSCDKNKLNVFSSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

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FIGURE 7

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACAT**TAG**

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR
RQDPQLKGI VTRLYCRQGYLQMHDPGALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 9

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCA
GACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCT
GTGTCCAGACTGAGGCCCCATTTGCATTGTTTAACATACTTAGAAAATGAAGTGTTTCAATTTT
TAACATTCTCCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGGCTAAGCAAAACCAGGT
GCTTGCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGGCGCTCTCCCCGTGTCCTCTCCA
CGACTCGCTCGGCCCCCTCTGGAATAAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGA
CGTGCCCCGAGCTCCTCCGGGGGTCCCGCCCGCGAGCTTTCTTCTCGCCTTCGCATCTCCTCC
TCGCGCGTCTTGGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTG
TCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGT
CAGGACAGTGTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATG
ATGTGTGTTAACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGG
GCCCTACTCGAACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCAC
TCTCAGCTCCAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATAACAGATG
GATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCC
CACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGC
TTCTGGAAGGCCAGTGCTTAGACATTGATGAATGTGCTATGGTTACTGCCAGCAGCTCTGT
GCGAATGTTCTGGATCCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGG
AAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCTGCGTGCAAACCTGCGTCA
ACACCTACGGCTCTCTCATCTGCCGCTGTGACCCAGGATATGAACCTGAGGAAGATGGCGTT
CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAA
CCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAA
GCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGC
TACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAG
GATCAGTGATAACCGCTGTATGTGTCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTA
CCATCTTGTACCGGGACATGGACGTGGTGTGTCAGGACGCTCCGTTCCCGCTGACATCTTCCAA
ATGCAAGCCACGACCCGCTACCCTGGGGCCTATTACATTTTCCAGATCAAATCTGGGAATGA
GGGCAGAGAATTTTACATGCGGGCAAACGGGCCCCATCAGTGCCACCCTGGTGATGACACGCC
CCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTGGAATGATCACTGTCAACACTGTCTATC
AACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTGCGCAGTACCCATTCTTGAGC
CTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGACAGGAGAAGAGAGGAAA
TAACAGAGAGAATGAGAGCGACACAGACGTTAGGCATTTCCCTGCTGAACGTTTCCCCGAAGA
GTCAGCCCCGACTTCCTGACTCTCACCTGTACTATTGCAGACCTGTACCCCTGCAGGACTTG
CCACCCCCAGTTCCTATGACACAGTTATCAAAAAGTATTATCATTGCTCCCCTGATAGAAGA
TTGTTGGTGAATTTTCAAGGCCTTCAGTTTATTTCCACTATTTTCAAAGAAAATAGATTAGG
TTTGCGGGGGTCTGAGTCTATGTTCAAAGACTGTGAACAGCTTGCTGTCACTTCTTCACCTC
TTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCAAAGACCCGGGAGCTGGCGGGGAACCTT
GGGAGTAGCTAGTTTGCTTTTTCGTACACAGAGAAGGCTATGTAAACAAACCACAGCAGGA
TCGAAGGGTTTTTAGAGAATGTGTTTCAAACCATGCCTGGTATTTTCAACCATAAAAGAAG
TTTCAGTTGTCTTAAATTTGTATAACGGTTTAAATCTGTCTTGTTCATTTTGAGTATTTT
AAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCC
AAACCCAGTCTCCTCTCCATTTTAGCCCAGTGTTTTCTTTGAGGACCCCTTAATCTTGCTTT
CTTTAGAATTTTTACCCAATTGGATTGGAATGCAGAGGTCTCCAACTGATTAAATATTTGA
AGAGA

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FIGURE 10

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ
NGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQ
CVDVDECATDSHQCNPTQICINTEGGYTCSCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPG
SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDM
DECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQG
GFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPF TILYRDMDVVSGRSVPADIFQMATT
RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGS
SVIRLRIYVSQYPF

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

FIGURE 11

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGAACACAGGTCCTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTG
GAAGGAGGGAGTGCAGGGGCTGCCCCGGGCTCCTCCCTGCCGCCTCCTCTCAGTGGATGGTT
CCAGGCACCTGTCTGGGGCAGGGAGGGACAGGCCTGCACATCGAAGGTGGGGTGGGACCA
GGCTGCCCCCTCGCCCCAGCATCCAAGTCCTCCCTTGGGGCGCCCGTGGCCCTGCAGACTCTCA
GGGCTAAGGTCTCTGTTGCTTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGT
AGCTTGAAGGAGGCACCA**ATG**CAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTG
GCTCAGGCCTGCCCTGAGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTG
TGCCTACCGCGACCTAGAATCCGTGCCGCCTGGCTTCCCGGCCAATGTGACTACACTGAGCC
TGTGAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCAGGGAGGTGCCCTGCTGCAG
TCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCTCTCTGAG
CCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGC
ACAACCTCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGC
GACGCCTTCCGCAGCCTCCGTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACAC
ATTGGCCGAGGGCACCTTACCCCCGCTACCGCGCTGTCCACCTGCAGATCAACGAGAACC
CCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCCTGACCACGGCCGTGTCC
ATCCCGGAGCAGGACAACATCGCCTGCACCTACCCCCATGTGCTCAAGGGTACACCGCTGAG
CCGCCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGG
ATGGTGCCGAGCTGCGGCCTGGTTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCG
GCCCCCTCAGCTTCACTGGCACATCCAGATAACCCAGTGGCATTGTGGAGATCACCAGCCCCAA
CGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCCCTGTGGCCAGCTCCCAGCCGCGCTTCC
AGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC
AGCTGCCTGGCCACCAATGAGCTGGGCAGTGTGAGAGCTCAGTGGACGTGGCACTGGCCAC
GCCCCGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGTTGAGGGAA
AGGGCTGCTATACGGTTGACAACGAGGTGCAGCCATCAGGGCCGGAGGACAATGTGGTCATC
ATCTACCTCAGCCGTGCTGGGAACCCCTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCT
GCCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCCTCTTCTTCTTCTCCTCACCTCCTTCT
AGCCCCACCCAGGGCTTCCCTAACTCCTCCCCTTGCCCCCTACCAATGCCCCCTTTAAGTGCTG
CAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCT
CCTTCTAATCTCTTCTAGAGCACCTGCTATCCCCAAGTCTAGACCTGCTCCAAACTAGTGA
CTAGGATAGAATTTGATCCCCTAACCTCACTGTCTGCGGTGCTCATTGCTGCTAACAGCATTG
CCTGTGCTCTCCTCTCAGGGGCAGCATGCTAACGGGGCGACGTCCTAATCCAAGTGGGAGAA
GCCTCAGTGGTGGAATTCCAGGCACTGTGACTGTCAAGCTGGCAAGGGCCAGGATTGGGGGA
ATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAATGGGAGAGGAGGATGG
GAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCT
CCTTGCTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAA
TGTGGGGATCCAGGATGGCCTTCCCTCCTTACCCTTCCCTCAGCCTGCAACCTCTAT
CCTGGAACCTGTCCTCCCTTTCTCCCCAAGTATGCATCTGTTGTCTGCTCCTCTGCAAAGGC
CAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATGCCAAAAAAAAAAAAAAAAA
AAGGGCGGCCGCGACTCTAGAGTCGACCT

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FIGURE 12

MQELHLLWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFPANVTTLSSLNRL
PGLPEGAFREVPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSAL
QLLKMSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCTC
GIVWLKTWALTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELR
PGFVLALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANG
SLIPDFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTV
DNEVQPSGPEDNVVVIYLSRAGNPEAAVAEGVPGQLPPGLLLLQSLLLFFFLTSF

Important features of the protein:

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites.

amino acids 51-55, 120-124, 309-313

Tyrosine kinase phosphorylation site.

amino acids 319-326

N-myristoylation sites.

amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329,
334-340, 350-356, 394-400

Amidation site.

amino acids 355-359

Leucine rich repeats.

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

Leucine rich repeat C-terminal domain.

amino acids 180-230

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FIGURE 14

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
 MAPFTHDFRKAQQORMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
 GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
 RGGGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
 TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPV
 EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
 PESNYIW

Signal sequence.

amino acids 1-28

N-glycosylation sites.

amino acids 88-92, 245-249

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

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FIGURE 16

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCCEFQYSHKPLPWTWVRSYEFTSNSCSQRAV
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

Important features of the protein:

Signal peptide:

amino acids 1-23

N-myristoylation sites.

amino acids 3-9, 26-32

Amidation site.

amino acids 68-72

Small cytokines (intecrine/chemokine).

amino acids 23-88

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FIGURE 17

GCGAGAACCTTTGCACGCGCACAAACTACGGGGACGATTTCTGATTGATTTTTTGGCGCTTTTCGATCCACCCTCC
TCCCTTCTC**ATG**GGGACTTTGGGGACAAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGC
CAGGACAGCGTCGGGAACCAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTTCGTCGTCTTCATCGTCGCGG
TTCTGCTGCCGGTCCGGGTTGACTCTGCCACCATCCCCGGCAGGACGAAGTTCCCCAGCAGACAGTGGCCCCA
CAGCAACAGAGGGCGAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTG
TAACCCGTGCACAGAGGGTGTGGATTACACCATTTGCTTCCAACAATTTGCCTTCTTGCTGCTATGTACAGTTT
GTAAATCAGGTCAAACAAATAAAAGTTTCTGTACCACGACCAGAGACACCGTGTGTCACTGTGAAAAAGGAAGC
TTCCAGGATAAAAACTCCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTCAG
TAATTGTACGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAACCCAGCAG
CGGAGGAGACAGTGACCACCATCCTGGGGATGCTTGCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTA
GTCATCATTTTTAGCTGTGGTTGTGGTTGGCTTTTCATGTGCGAAGAAATTCATTTTACCTCAAAGGCATCTG
CTCAGGTGGTGGAGGAGTCCCGAACGTGTGCACAGAGTCCTTTTCCGGCGGGCTTCATGTCTTCACGAGTTC
CTGGGGCGGAGGACAATGCCCGCAACGAGACCCTGAGTAACAGATACTTGCAGCCACCCAGGTCTCTGAGCAG
GAAATCCAAGGTGAGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCGCCAGAGGAGCCACAGCGTCTGCT
GGAACAGGCAGAAGCTGAAGGGTGTGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACA
TCAGCACCTTGCTGGATGCCTCGGCAACACTGGAAGAAGGACATGCAAGGAAACAATTCAGGACCAACTGGTG
GGTCCGAAAAGCTCTTTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCTGCCTG**TGA**AAGAATCTCTCAG
GAAACCAGAGCTTCCCTCATTTACCTTTTCTCTACAAAGGGAAGCAGCCTGGAAGAAAACAGTCCAGTACTTGA
CCCATGCCCCAACAACTCTACTATCCAATATGGGGCAGCTTACCAATGGTCCCTAGAATTTGTTAACGCACTT
GGAGTAATTTTTATGAAATACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCCTGGCTGCATAGT
TATACGATTGTGTATTAAGGGTCGTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGATAG
GCTGAGGCAGGTGGATTGCTTGAGCTCGGGAGTTTGAGACCAGCCTCATCAACACAGTGAAACTCCATCTCAAT
TTAAAAAGAAAAAAGTGGTTTTAGGATGTCATTCTTTGCAGTTCTTCATCATGAGACAAGTCTTTTTTTCTGC
TTCTTATATTGCAAGCTCCATCTCTACTGGTGTGTGCATTTAATGACATCTAACTACAGATGCCGCACAGCCAC
AATGCTTTGCCTTATAGTTTTTAACTTTAGAACGGGATTATCTTGTTATTACCTGTATTTTCAGTTTCGGATA
TTTTTGACTTAATGATGAGATTATCAAGACGTATGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTC
GACTTAGAGTTTTGAGCTTTAAGATAGGATTATTTGGGGCTTACCCCACTTAATTAGAGAAACATTTATATTG
CTTACTACTGTAGGCTGTACATCTCTTTTCCGATTTTTGTATAATGATGTAAACATGGAAAAACTTTAGGAAAT
GCACTTATTAGGCTGTTTACATGGGTGCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATAACTAGT
GACGGAGGGAGAAATCCTCCCTCTGTGGGAGGCACTTACTGCATTCCAGTTCTCCCTCCTGCGCCCTGAGACTG
GACCAGGGTTTGATGGCTGGCAGCTTCTCAAGGGGCAGCTTGTCTTACTTGTAAATTTTAGAGGTATATAGCCA
TATTTATTTATAAATAAATATTTATTTATTTATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGC
CTGGTATCTTTGGGAAGCCATGTGTCTGGTTTGTCTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTG
CACAGCAGATGAGGACAGTGAGAATTAAGTTAGATCCGAGACTGCGAAGAGCTTCTCTTCAAGCGCCATTACA
GTTGAACGTTAGTGAATCTTGAGCCTCATTTGGGCTCAGGGCAGAGCAGGTGTTTATCTGCCCGGCATCTGCC
ATGGCATCAAGAGGGAAGAGTGGACGGTGTCTGGGAATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGC
CCCTCTCGCTTCTGGTGGTCTGTGAACGTGAGTCCCTGGGATGCCTTTTAGGGCAGAGATTCCTGAGCTGCGTTT
TAGGGTACAGATTCCTGTTTGGAGAGCTTGCCCCCTCTGTAAGCATCTGACTCATCTCAGAGATATCAATTCT
TAAACACTGTGACAACGGGATCTAAAATGGCTGACACATTTGTCTTGTGTACGTTCCATTATTTTATTTAAA
AACCTCAGTAATCGTTTTAGCTTCTTCCAGCAAACCTCTTCTCCACAGTAGCCAGTCTGTTGGTAGGATAAATTA
CGGATATAGTCATTCTAGGGGTTTCAGTCTTTTCCATCTCAAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTG
GCTGGGACAAAGTTAGAATGCCTGAAGTTCGCACATTCAGATTGTTGTGTCCATGGAGTTTTAGGAGGGGATG
GCCTTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATCTGGCGTCCACACCTTGTCCCTGCACTTCTG
GATGACACAGGGTGTGCTGCTGCTCCTAGTCTTTGCCTTTGCTGGGCCTTCTGTGCAGGAGACTTGGTCTCAAAG
CTCAGAGAGAGCCAGTCCGGTCCAGCTCCTTTGTCCCTTCTCAGAGGCCTTCTTGAAGATGCATCTAGACT
ACCAGCCTTATCAGTGTTTAAGCTTATTCCTTTAACATAAGCTTCTGACAACATGAAATTTGTTGGGGTTTTTT
GGCGTTGGTTGATTTGTTTAGGTTTTGCTTTATACCCGGGCCAAATAGCACATAACACCTGGTTATATATGAAA
TACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 18

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQD
 EVPQQTVA PQQRRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG
 QTNKSSCTTTRDTVCQCEKGSFQDKNSPEMCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAA
 SSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVIILAVVVVGFSCRKKFISYLGKICSGGG
 GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAELTGVTVES
 PEEPQRLLEQAEAGCQRRRLLPVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKL
 FYEEDEAGSATSCL

Important features of the protein:

Transmembrane domains:

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,
 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

FIGURE 19

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTGTAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

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FIGURE 20

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Important features of the protein:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

FIGURE 21

CCGGGGAGGGGAGGGCCCGTCCCGCCCCCTCCCCGTCTCTCCCCGCCCCCTCCCCGTCCCTCCC
GCCGAAGCTCCGTCCCGCCCCGCGGGCCGGCTCCGCCCTCACCTCCCGGCCGCGGGCTGCCCTC
TGCCCGGGTTGTCCAAG**ATG**GAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGCTCCTGCTG
TTCGTGGCGCTACCCGCCTCCGGCTGGCTGACGACGGGCGCCCCCGAGCCGCCGCCGCTGTC
CGGAGCCCCACAGGACGGCATCAGAATTAATGTAACCTACACTGAAAGATGATGGGGACATAT
CTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAAATGACTTA
CCTGTAAATAGTGGTGTAAACCCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAAATCT
TGAAAATTTGGAGGAAAAAGAATATTTTGGAAATTGTCAGTGTAAAGGATTTTAGTTTCATGAGT
GGCCTATGACATCTGGTTCCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT
GATGGAAAACAAGTTCAGCAAAAGGATGTCACTGAAATTGATATTTTAGTTAAGAACCGGGG
AGTACTCAGACATTCAAACCTATACCCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTTCTC
GAGACAGTGACATTTTATTTACCCTTCCTAACCTCTCCAAAAAAGAAAGTGTTAGTTCACTG
CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAAACCACTGTAGATGAAGATGTTTTACC
TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCCGCCATCTTCATATAAGGTAATGTGTC
AGTGGATGGAAAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTCCAGTATTC
TTTCAGTTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT
AAAGGTGTTTTTTCCAGTTTCTGAATACAAAGGAATTCTTCAGTTGGATAAAGTGACGTCA
TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA
GATAAAACATGTATTT**TAA**ACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCC
AAATTTGCCACTTGAATATAATTTTCTTTAAATCGTT

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FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783
><subunit 1 of 1, 330 aa, 1 stop
><MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGSLALRLLLFVALPASGWLTTGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVV
LNITYESGQVYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQQKDVTEIDILVKNRGVLRHSNYTLPLEESMLYSISRSDIL
FTLPNLSSKKESVSSLQTTSSQYLIRNVETTVDVDVLPGKLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFWSNVFPVFFQFLNIMVVGITGAAVVITILKVFFPVSEYKGILQLDKVDVIPVTAI
NLYPDGPEKRAENLEDKTCI
```

Important features of the protein:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 266-284

Leucine zipper pattern.

amino acids 155-176

N-glycosylation sites.

amino acids 46-49, 64-67, 166-169, 191-194

FIGURE 23

CGTCTCTGCGTTTCGCC**ATG**CGTCCCGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGG
CCCTGGCTTGGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGT
GTTTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCAC
CCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGG
GGAACAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCACTGCCTTCCCTGCAAAGATTCTG
TGCGACGGCGTGAGTGCGGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCCGCGCTG
CGAGTGCGCGCCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCG
CCACCTACCGCGACGAGTGCGAGCTGCGCGCCGCGCGCTGCCGCGGCCACCCGGACCTGAGC
GTGCGTTCGTGGACCAGACGGGCGAGCGCCACTGCGTGCTGTGTGTCGAGCGGGCGCCCTGCCCTG
TGCCCTCCAGCCCCGGCCAGGAGCTTTGCGGCAACAACAACGTCACCTACATCTCCTCGTGC
CACATGCGCCAGGCCACCTGCTTCCCTGGGCCGCTCCATCGGCGTGCGCCACGCGGGCAGCTG
CGCAGGCACCCCTGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAAGTTCGTG**T**
GAGCCTGCAGGACAGGCCTGGGCCTGGTGCCGAGGCCCCCCATCATCCCTGTTATTTATT
GCCACAGCAGAGTCTAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTTCGGACCACTT
GGGGATCCCAGAACCTCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCC
GGCTGGTGGGTGGGATAGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCT
AGGATGCCCCAGCCCTACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTT
TGGGGATAAACCTATTAATTATTGCTACTATCAAGAGGGCTGGGCATTTCTCTGCTGGTAATT
CCTGAAGAGGCATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGT
CTAGCCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAG
TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAG
CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG
GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG
GGTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGCGTGTGGGA
CCTCAGAACACTGTGACCTTAGCCCAGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGC
CACCATTCCCTGCCAGCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT
CCTGTGAAGGCCATTGAGAAATGCCAGTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCC
TGACACGGGCTGTGCTTGGCCACAGAACCACCCAGCGTCTCCCCTGCTGCTGTCCACGTCAG
TTCATGAGGCAACGTCGCGTGGTCTCAGACGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGC
ACTGTGTCCGGCGGAGCCAAGTCCACTCTGGGGGAGCTCTGGCGGGGACCACGGGCCACTGC
TCACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATGTGTGACATCCGGAGT
CCTGGAGCCGGGTGTCCCAGTGGCACCCTAGGTGCCTGCTGCCTCCACAGTGGGGTTTACA
CCCAGGGCTCCTTGGTCCCCACAACCTGCCCCGGCCAGGCCTGCAGACCCAGACTCCAGCC
AGACCTGCCTCACCCACCAATGCAGCCGGGGGCTGGCGACACCAGCCAGGTGCTGGTCTTGGG
CCAGTTCTCCACGACGGCTCACCC'TCCCCCTCCATCTGCGTTGATGCTCAGAATCGCCTACC
TGTGCCTGCGTGTAACCACAGCCTCAGACCAGCTATGGGGAGAGGACAACACGGAGGATAT
CCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGCTTGGGCATCCTCCTCCAGCCTCCTC
CAGCCCCCAGGCAGTGCCTTACCTGTGGTGCCCAGAAAAGTGCCCCCTAGGTTGGTGGGTCTA
CAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCCCTGCCTCACCAAGGAAATAAAGA
CTCAAGCCATAAAAAAA

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FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGPLWPLPWGALAWAVGVSSMSGNPAPGGVCWLQQGQEATCSLVLQTDVTRAEC
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVCEGPGKACRMLGGRPRCECAPD
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSCHEHVVCPRPQSCVVDQ
TGAHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE
EPPGGESAEEEEENFV

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation sites.

amino acids 73-77, 215-219

Osteonectin domain proteins.

amino acids 97-130, 169-202

FIGURE 25

TGCAGAGCTTGTGGAGGCC**ATG**GGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGT
TGTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGAT
AAAATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAA
ATTTGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCGCCTGGCTA
CCATGATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTCATCCATCCTTTAAATCTG
CACATGAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACT
GGGGATATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGA
TTAAATTAGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTG
TTAGACAAGTTCATGAGGATCTACCGCTACCACTCTCATGACTATGCCTTCAGTAGTGTCGA
AAAATTACTTCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTG
AAACCTTGCAAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATG
AGGGTCAATTATGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCCTG
TTCTGATTCTGGCCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGC
AGGCATCCAAAAGCAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACC
AAGTACACAGGAAATCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAAC TGAGACTCG
TTCAGACTTCTATGACATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTA
CTTTTCTCAACTTTGATCCTCCAATTGAGGAATTCATCAATATTATCAACATATAGTGACA
ACTTTAGTTAAGGGGGAATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGG
CCTTAATACAGTTTTTAACCACTGATAATTCAGATTTGTTTCATTAACAGTATTGGGATTGTGC
CCTCTGTGAGAGAAAAGGAAGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATC
TTTTCCCAAGAACTCTTACTAAAGCACAAATTTTAAAGCTCTTTCTGTCTATGATTATGC
TGTGAAGAAGCCATGGCTTGCATATCCTCACTATAAGCCCCCGAGAAATGCCCTCTATCA
TTCTCCATGATCGACTTTATTACCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATG
AGTGCCATTGCAGCCCACAACGCTGCACTCCTTGCCTATCACCGCTGGAACGGGCACACAGA
CATGATTGATCAGGATGGCTTATATGAGAACTTAAACTGAACTA**TGA**AGTGACACACTCC
TTTTTCCCCTCCTAGTTCCAAATGACTATCAGTGGCCAAAAAAGAACAAAATCTGAGCAGAGA
TGATTTTGAACCAGATATTTTGCCATTATCATTGTTTAATAAAAGTAATCCCTGCTGGTCAT
AGGAAAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880

<subunit 1 of 1, 505 aa, 1 stop

<MW: 56640, pI: 6.10, NX(S/T): 4

MGRVVAELVSSLLGLWLLLCSCGCPEGAE LRAPPDKIAIIGAGIGGTS AAYYLRQKFGKDVK
IDLFEREEVGGRLATMMVQGGQEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGE
TLVFEESNWFIIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHAL
GGDDFLGMLNRTLLET LQKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLW
AVEGGNKLVC SGLLQASKSNLISGSVMYIEEKTKTKYTGNPTKMYEVVYQIGTETRSDFYDI
VLVATPLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFG LNTVLT
TDNSDLFINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKLFLSYDYAVKKPWL
AYPHYKPPKEKCP SII LHDRLYYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDG
LYEKLKTEL

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23, 232-243

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FIGURE 27

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGAC**ATGAT**
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAAATG
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCTTCTTT
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAGACTTATTTCAGTCAGAGCTA**TAA**
GAGATGATGGAAAAAAGCCTTCACTTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAAATATTACTATTTAGTTTTTTTA
ATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTAAATCTGA

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FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTVSSNLAIAIKKEKRPPQTL SRGWGDDITWVQTYEEGLFYAQKSKKPL
MVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNL MHETTDKNLSPDGQYVPRIMFVDP
SLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

Important features:

Signal peptide:

amino acids 1-23

N-myristoylation site.

amino acids 51-57

FIGURE 29

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA
AAGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCA
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAG
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCAC
CAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCTTATTCCAATACCTGAATCT
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAA
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA
ATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9700, pI: 9.55, NX(S/T): 0

MKKVLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFP
WFRNFIPIPIESAPTTPLPSEK

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

FIGURE 31

CGGACGCGTGGGCGGGCGCGCCGGGAGGGACCGGCGGCGGC**ATG**GGGCCGGGGGCCCTGGGAT
 GCGGGCCCCGTCTCGCCGCTGCTGCCGCTGTTGCTGCTGCTCGGCCTGGCCCCGCGGCGCCGC
 GGGAGCGCCGGGCCCCGACGGTTTAGACGTCTGTGCCACTTGCCATGAACATGCCACATGCC
 AGCAAAGAGAAGGGAAGAAGATCTGTATTTGCAACTATGGATTTGTAGGGAACGGGAGGACT
 CAGTGTGTTGATAAAAATGAGTGCCAGTTTGGAGCCACTCTTGTCTGTGGGAACACACATC
 TTGCCACAACACCCCCGGGGGCTTCTATTGCATTTGCCTGGAAGGATATCGAGCCACAAACA
 ACAACAAGACATTCAATCCCAACGATGGCACCTTTTGTACAGACATAGATGAGTGTGAAGTT
 TCTGGCCTGTGCAGGCATGGAGGGCGATGCGTGAACACTCATGGGAGCTTTGAATGCTACTG
 TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCCACCCGACCACCGATGCCACAT
 CATGCACAGAAATAGACTGTGGTACCCCTCCTGAGGTTCCAGATGGCTATATCATAGGAAAT
 TATACGTCTAGTCTGGGCAGCCAGGTTGTTATGCTTGCAGAGAAGGATTTCTTCAGTGTTC
 AGAAGATACAGTTTCAAGCTGCACAGGCCTGGGCACATGGGAGTCCCCAAAATTACATTGCC
 AAGAGATCAACTGTGGCAACCCTCCAGAAATGCGGCACGCCATCTTGGTAGGAAATCACAGC
 TCCAGGCTGGGCGGTGTGGCTCGCTATGTCTGTCAAGAGGGCTTTGAGAGCCCTGGAGGAAA
 GATCACTTCTGTTTGCACAGAGAAAGGCACCTGGAGAGAAAGTACTTTAACATGCACAGAAA
 TTCTGACAAAGATTAATGATGTATCACTGTTTAAATGATACCTGTGTGAGATGGCAAATAAAC
 TCAAGAAGAATAAACCCCAAGATCTCATATGTGATATCCATAAAAGGACAACGGTTGGACCC
 TATGGAATCAGTTCGTGAGGAGACAGTCAACTTGACCACAGACAGCAGGACCCAGAAAGTGT
 GCCTAGCCCTGTACCCAGGCACCAACTACACCGTGAACATCTCCACAGCACCTCCCAGGCGC
 TCGATGCCAGCCGTCATCGGTTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGGAAG
 TTTCAATATTTCAATATTTAATGAACTTGTTTGAATTTGAACAGGCGTTCTAGGAAAGTTG
 GATCAGAACACATGTACCAATTTACCGTTCTGGGTCAGAGGTGGTATCTGGCTAACTTTTCT
 CATGCAACATCGTTTAACTTCACAACGAGGGAACAAGTGCCTGTAGTGTGTTTGGATCTGTA
 CCCTACGACTGATTATACGGTGAATGTGACCCTGCTGAGATCTCCTAAGCGGCACTCAGTGC
 AAATAACAATAGCAACTCCCCCAGCAGTAAACAGACCATCAGTAACATTTTCAAGATTTAAT
 GAAACCTGCTTGAGATGGAGAAGCATCAAGACAGCTGATATGGAGGAGATGTATTTATTCCA
 CATTGTTGGGGCCAGAGATGGTATCAGAAGGAATTTGCCCAGGAAATGACCTTTAATATCAGTA
 GCAGCAGCCGAGATCCCGAGGTGTGCTTGGACCTACGTCCGGGTACCAACTACAATGTCAGT
 CTCCGGGCTCTGTCTTCGGAACCTTCTGTGGTTCATCTCCCTGACAACCCAGATAACAGAGCC
 TCCCCTCCCGGAAGTAGAATTTTTTACGGTGCACAGAGGACCTCTACCACGCCTCAGACTGA
 GGAAAGCCAAGGAGAAAAATGGACCAATCAGTTCATATCAGGTGTTAGTGTCTCCCCTGGCC
 CTCCAAAGCACATTTTCTTGTGATTCTGAAGGCGCTTCTCCTTCTTTAGCAACGCCTCTGA
 TGCTGATGGATACGTGGCTGCAGAACTACTGGCCAAAGATGTTCCAGATGATGCCATGGAGA
 TACCTATAGGAGACAGGCTGTACTATGGGGAATATTATAATGCACCCCTTGAAAAGAGGGGAGT
 GATTACTGCATTATATTACGAATCACAAGTGAATGGAATAAGGTGAGAAGACACTCCTGTGC
 AGTTTGGGCTCAGGTGAAAGATTCGTCACTCATGCTGCTGCAGATGGCGGGTGTGGACTGG
 GTTCCCTGGCTGTTGTGATCATTCTCACATTCCTCTCCTTCTCAGCGGT**GTGA**TGGCAGATG
 GACACTGAGTGGGGAGGATGCACTGCTGCTGGGCAGGTGTTCTGGCAGCTTCTCAGGTGCC
 GCACAGAGGCTCCGTGTGACTTCCGTCCAGGGAGCATGTGGGCCTGCAACTTTCTCCATTCC
 CAGCTGGGCCCCATTCTTGATTTAAGATGGTGGCTATCCCTGAGGAGTCACCATAAGGAGA
 AACTCAGGAATTCTGAGTCTTCCCTGCTACAGGACCAGTTCTGTGCAATGAACTTGAGACT
 CCTGATGTACACTGTGATATTGACCGAAGGCTACATACAGATCTGTGAATCTTGGCTGGGAC
 TTCTCTGAGTGATGCCTGAGGGTCAGCTCCTCTAGACATTGACTGCAAGAGAATCTCTGCA
 ACCTCCTATATAAAAGCATTTCTGTTAATTCATTCAGAATCCATTCTTTACAATATGCAGTG
 AGATGGGCTTAAGTTTGGGCTAGAGTTTGAAGGAGGTGATTGAAAAGAGAAACA
 GTGACGTAGGCAAATGTTTCAAGCACTTTAGAAACAGTACTTTTCCCTATAATTAGTTGATAT
 ACTAATGAGAAAATATACTAGCCTGGCCATGCCAATAAGTTTCTGCTGTGTCTGTTAGGCA
 GCATTGCTTTGATGCAATTTCTATTGTCTATATATTCAAAGTAATGTCTACATTCCAGTA
 AAAATATCCCGTAATTAAAAA

FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96031
><subunit 1 of 1, 747 aa, 1 stop
><MW: 82710, pI: 6.36, NX(S/T): 18
MGRGPWDAGPSRLLPLLLLLGLARGAAGAPGPDGLDVCATCHEHATCQQREGKKICICNYG
FVGNGRTOCVDKNECQFGATLVCGNHTSCHNTPGGFYCICLEGYRATNNNKTFIPNDGTFCT
DIDECEVSGLCRHGGRCVNTHGSEFECYCMDGYLPRNGPEPFHPTTDATEIDCGTPPEVP
DGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTWESPCLHLCQEINCGNPPEMRHA
ILVGNHSSRLGGVARYVCQEGFESPGGKITSVCTEKGTWRESTLTCTEILTAKINDVSLFNDT
CVRWQINSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPÉVCLALYPGTNYTVNI
STAPRRSMPAVIGFQTAEDVLDLEDGSEFNISIFNETCLKNRRSRKVGSEHMYQFTVLGQR
WYLANFSHATSFNFTTREQVPVVCCLDLYPTTDYTVNVTLRLSPKRHSVQITIATPPAVKQTI
SNISGFNETCLRWSIKTADMEEMYLFIHWQQRWYQKEFAQEMTFNISSSSRDPEVCLDLRP
GTNYNVSLRALSSELPPVVISLTTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQ
VLVLPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAQDVPDDAMEIPIGDRLYYGEYYN
APLKRGSYCIILRITSEWNKVRRHSCAVWAQVKDSSLMLLQMAGVGLGSLAVVILTFLSF
SAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 718-740

N-glycosylation sites.

amino acids 87-91, 112-116, 193-197, 253-257, 308-312, 348-352, 367-371, 371-375, 402-406, 407-411, 439-443, 447-451, 470-474, 498-502, 503-507, 542-546, 563-567, 645-649

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 478-482, 686-690, 705-709

Tyrosine kinase phosphorylation site.

amino acids 419-427

N-myristoylation sites.

amino acids 22-28, 35-41, 65-71, 86-92, 96-102, 120-126, 146-152, 192-198, 252-258, 274-280, 365-371, 559-565, 688-694, 727-733.

Amidation site.

amino acids 52-56

Aspartic acid and asparagine hydroxylation sites.

amino acids 91-103, 141-153.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 624-635

Cytochrome c family heme-binding site signature.

amino acids 39-45

Calcium-binding EGF-like domain proteins pattern proteins.

amino acids 85-106, 135-156

Receptor tyrosine kinase class V proteins:

amino acids 389-422

FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
GGCTGTCTCTGGGGTCTGGCTCTGCCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCAGAAGCAGAGACCAGGGGAGCCAA
GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA
TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG
GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTCACAGCCTCTGCCGAGACCCTGTCC
ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTTC
CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCT
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC
GAGGCCGACCACAGACG**TGAG**TGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCCACGCCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
CGGAGTGTATGTATGGGGAGGGGCTTCACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA
TTAAAATTCACTCAGTGTGGCCCCAAAAAAA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722
><subunit 1 of 1, 482 aa, 1 stop
><MW: 49060, pI: 4.74, NX(S/T): 4
MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
TTVQTITGSDPEEAI FDTLCTDDSS EAKTLTMDILT LAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTNI
EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTSRD
PLPSVPPTTTN SSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-88

N-myristoylation sites.amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,
314-320, 349-355, 386-392, 397-403, 449-455**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

FIGURE 35

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAG
GCC**ATG**CTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCA
GGCAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC
CCCAGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCAGGATCGCGAGGCAGCA
GCGACCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGT
ACTTCGCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT
CCTGCCTGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA
TTGGCCCAGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA
ACTGGCTCTGTTCTGGTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA
AAATGTTTGTGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGAT
GTAGCTAAGGATTGGAATGACAACCCCCGGAAAAATTTCTGGGTATTCTCCTGGAGATACTGGT
CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT
GCTCCCTTCATGCTTCCCTGCTGGTGGTGA CTCTCAACCCTGATCAGTGCCACCCTTCTCGG
AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCA
GCTATTTCATTA ACTTCCGGGACCTGGGTTGGCACAAGTG GATCATTGCCCCCAAGGGGTTCA
TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAAT
TATGCTTTTCATGCAAGCCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTAT
CCCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTAC
GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGG**TAG**GATGTCAGAAATGGGAAT
AGAAGGAGTGTTCTTAGGGTAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTA
GATCGAAATGTC

FIGURE 36

MLRFLPDLAFSFLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVYPYILKKIFQDREAAA
TTGVSRLCYVKELGVRGNVLRFLPDQGGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL
AQLGLDLGPNSYYNLGPELELALFLVQEPHVWGQTTPKPGKMFVLRVWPWPQGAVHFNLLDV
AKDWNNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRK
RRAAIPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECPFSLTISLNSSNY
AFMQALMHAVDPEIPQAVCIPTKLSPIISMLYQDNNDNVILRHYEDMVVDECGCG

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

FIGURE 37

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTTCGCAGAGAC
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTT
TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGGGACGGAGGGCCCCGGCAGGAAG**ATG**GGC
TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCTTTGCTCTGGCCTGGT
CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC
GGCGACCGCGGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG
ATCGAGGCCTCCAAGGGAAATATGGCAAACAGGCTCAGCAGGGGGCCAGGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGTACTCTCG
ACACGGAGTTTCGTGAACCTCTACGACCACTTCAACATGTTTACCGGCAAGTTCTACTGCTAC
GTGCCCCGGCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCAAGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTTCGCGCAGGTGGGCGACCGCAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCC**TAG**CTGGCCGGCCACCTCCTTTCTCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGATCCCTGGACTCCGACTC
CCTGGCTTTGGCATTTCAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC
GAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGCGGCACCGCGGCTCCAGTCTTTGGAAATA
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAG
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGGCCGGGGGCAGG
AAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT
GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCCCTGGCATCGGCT
TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCCACTGCCCT
CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCCGCTTGCTGTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCAGGATTCAGTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCCGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
GTGTCTCCACGGTGTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC
ATAGCCCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC
CCCAAACCCCCGCTGCCTCTCTTCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC
TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
GCTGCTTAAGCTCCCCCAGCTCTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

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FIGURE 38

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIIFSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 39

GAATTCGGCACGAGGGAAGAAGAGAAAGAAAATCTCCGGGGCTGCTGGGAGCATATAAAGAA
GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGAC**ATGG**CTG
CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCCTTAACCTAGGCATCTTCGTCCGTCCCTGT
GACACTCAAGAGCTACGATGTCTGTGTATTTCAGGAACACTCTGAATTCATTCCTCTCAAAC
CATTA AAAATATAATGGTGATATTCGAGACCATTTACTGCAACAGAAAGGAAGTGATAGCAG
TCCCAAAAATGGGAGTATGATTTGTTTGGATCCTGATGCTCCATGGGTGAAGGCTACTGTT
GGCCAATTACTAACAGGTTCCCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGGCAAT
GAAGCTTCTGTATAGTGTTGAGCATGAAAAGCCTCTATATCTTTTCATTTGGGAGACCTGAGA
ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC
AACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCC**TA**
AAAGCCACTCATGAGGCAAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTTGGCGTTCTCA
TTCTTATACTCTATTCCCGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT
TATTATAAATGTTTTATTTACTTAACTTCCTAGTGAATGTTTCACAGGTGACTGCTCCCCCAT
CCCCATTTCTTGATATTACATATAATGGCATCATATAACCCCTTTATTGACTGACAAACTACT
CAGATTGCTTAACATTTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG
TGCATCTCGGTGTAGAGCAAGGCTCCTTGTCTTCAGTGCCCCAGGGTGAAATACTTCTTTGA
AAAATTTTCATTCATCAGAAAATCTGAAATAAAAATATGTCTTAATTGAG

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FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
><subunit 1 of 1, 167 aa, 1 stop
><MW: 19091, pI: 7.48, NX(S/T): 1
MAAQGWSMLLLAVLNLGIFVRPCDTQELRCLCIQEHSEFIPLKLIKNIIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPPAMKLLYSVEHEKPLYLSFGR
PENKRIFPFPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 68-72

N-myristoylation site.

amino acids 69-75

Small cytokines (intercrine/chemokine) C-x-C subfamily signature

amino acids 40-85

FIGURE 41

CAGAC**ATG**GCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC
AGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGAAGAT
TCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCATCCCAG
CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTC
TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCCAGGG
CTGCAGGAAGGACAGGGGGGCGCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAAGGCTGCA
AGAGGACTGAGCGGTCACAGACCCCTAAAGGGCCA**TAG**CCCAGTGAGCAGCCTGGAGCCCTG
GAGACCCACACAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG
CTCAGGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACACTCTTTCTCCTGCTTTAAC
CACCCCATCTGCATTCCCAGCTCTACCCTGCATGGCTGAGCTGCCCACAGCAGGCCAGGTCC
AGAGAGACCGAGGAGGGAGAGTCTCCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCTT
TGAAGGAGAATCATCAGGACCCTGGACCTGATACGGCTCCCCAGTACACCCACCTCTTCCT
TGTAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCCNCCCCA

FIGURE 42

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLILVLAFGIPRTQGS DGG AQDCCLKYSQRKIPAKVVRSYRKQEP SLGCSI PAI
LFLPRKRSQAELCADPKELWVQQLMQHLDKTPSPQKPAQGCRKDRGASKTGKKGKGSKGCKR
TERSQTPKGP

Important features of the protein:

Signal peptide:

amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 67-71

N-myristoylation sites.

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

Amidation site.

amino acids 112-116

Small cytokines.

amino acids 51-91

FIGURE 43

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACCTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCATATTTTACCTATGA

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FIGURE 44

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA
```

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

GCTCCCAAGCCAAAGAACACCTCGGGGGCCGCTGCGCGGTGGGGAGGAGATTCCCCGAAACCCGGCCG
 CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA
 CAAGAAGCCGCCGCCTGCCTGCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
 GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
 TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG
 CCGCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
 GGCACCTCACAGCCCCGCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCC**ATG**CGGAGCGGGTGTGTGGTGGTCCACGTATGG
 ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGGCC
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC
 ACGGGCTCTCCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGC
 CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
 CGTGACACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGGCTGCTTCAGT
 ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
 TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
 CAGAGGCTTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
 AGGACCTCAGGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG
 GACCCATTTGGGCTTGTCACCGGACTGGAGGGCCGTGAGGAGTCCCAGCTTTGAGAAG**TAA**CT
 GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGGCTGTGGTACCTGCAGCGTGGGGGACG
 TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGTAACATATTCAGAGTTTTCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
 CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA
 GGTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
 TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTTCTCTAATTTTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTTAATTTTCAGGAACAGGTGATCCACTCTGTA
 AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATGATCTATATCTCTACTTCCAGGG
 ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAAGTACTGGAGCAGCATGCCCCACCAG
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTTCCC
 CTGAGGCTCAGTTCTGTCACTGGATGCTGTCTGAGATAACTTGCTGTCCCGGTGTCACCTGC
 TTCCATCTCCAGCCACACAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
 CCCAGGCCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
 TTGAAGACCCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
 CCTTTCCCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
 TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG
 TTTTGTATATTAAATGGAGTTTGTTTGT

FIGURE 46

MRS GCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALLRTVAIKGVHVSRYLCMGADGKMQLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

GTCTGTTCCCAGGAGTCCTTCGGCGGGCTGTTGTGTAGTGGCCTGATCGCG**ATG**GGGACAAAGGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGAGACACCACCAGACTCGTTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGGCAGTGCTGACATGCTCAGAACAAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACAGCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAATGTGGGGGTTCATCGTGGCAGCCGTCTTGTAACCCTGATTCTCCTGGGAATCTTGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCTGTTGGT**TGA**GCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTTACAGGATGCCTTATTTGTCTTCTACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTTAAAGTGTTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGCAGGAATCTGCACTCAACTGCCACCTGGCTGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAGGATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTCGGGATCAGCCTGACCAACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

FIGURE 48

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLS CAYSGFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRV TFLPTGITFKSV TREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

CCCACGCGTCCGAACCTCTCCAGCG**ATG**GGGAGCCGCCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACAACATAACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGGACCAAGCGCACAC
GGCGGCCCCAGCCCCTCACG**TAG**TCTGGGAGGCAGGGGGCAGCAGCCCCTGGGCCGCTCCC
CACCCCTTTCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTCAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTTTGTTTGTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCCTGC

FIGURE 50

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMATRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHA EKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 51

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATC**ATG**AAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTGGCTTTGTGAGTGAAGAC
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTT**TGA**TGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTAAAAAAGAAATTGAA
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGAACCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

52/75

FIGURE 52

MKTIQPKMHNSISWAIIFTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVG FVSEDEYL
EIQGITREQSGDYEC SASNDVAAPVVR RVKVTVNYPPISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Signal peptide:

amino acids 1-28

[illegible]

FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
```

```
><subunit 1 of 1, 440 aa, 1 stop
```

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
 AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
 ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGM
 NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
 GSQSGSSGSGSNGDNNNGSSSSGGSSSGSSSGSSSGSSSGSSSGSSSGSSGNSGGSRGDSGSESSW
 GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
 GSGDNYRGQGSWSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 55

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATGG**CAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC
AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 56

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 57

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTAT**TGAT**GAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCCTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTCAFTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAA

FIGURE 58

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHG EVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD SGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQC NVTLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTL PWPBKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP IPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

ACTTGGCCATCACCTGTGTGCCAGTGTGGAAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGATTTTGTCTGTTTATTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT
 TTCCGTACTTCAGAAATGGGCGCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCTCT
 GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
 CTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
 TGGATTTTCTGTCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
 AATATTCAGACCATTTTACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC
 TCAAATTTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAA
 TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
 AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
 CACCTCTCTCCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTGTGCAGGACAACCGAT
 AAACCAACTTCCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCCGATGCTGACTCAAGGGGTTTTTGTATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCCCTTGGTTTTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTCATGTGCCAAGGTCCTGAACAAGTCCGGG
 GGATGGCCGTCAGGGAATTAAATATGAATCTTTTTGTCTGTCCCACCACGACCCCCGGCCTG
 CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT
 TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCAGTGATGGCATA
 CAAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGGCATCGTTTCAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTGTTCAGAGGC
 CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCCACAGCATGGGCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
 CCAGAAGTGGAATAACAACCGGGGGCGGCGGAAGATGATTATTGCGAGGCGGCACCAAGA
 AGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTTCAGATCGTCTCTCTTAAATAACGAT
 CAACTCTTAAAGGAGATTTTTCAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTA
 CACAGATGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
 ACTGCCATACGTTGACAGCCAGAGGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAAGTG
 CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACTCTTTGCTTTTTTAAATCTT

FIGURE 60

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
 SRAALAQLLKLEELHLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
 PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSCPTTTPLPLFTP
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSMSGSPFLAGLIGGAVIFVLVVL
 LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
 DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
 522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 61

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCA**ATG**AACTGTTATTTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA
AAGTCAAGCAGCCAGTGCATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATTATTTTCTGTTGAACCAACAACAGGAGTCAATAAGAATATCTTCTAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAATCATTTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
GATTCGCAAACATTTGACATTATTACTAATCATGAAACTCAAGAAGGAATAGTTATATTTAA
AAAGAAAGTGGATTTTGGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTGA
AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC
ACTACAAGTAACCTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCCTTAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCATTTTGACTAATAGAAGTGGTTTAACTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTGCATTATGATCATA
TTTGGGTTTATTTTTTTTGAAGTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTCTGA
GAAAAGTGAAGATTTTCAAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
CCCCCTCTTTTGAATCCCTCCAGACCTACGCTTTTGGAGGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAGATTAGCATGCATGTTGGTTCTGCAGTGCAGTCAAATAAT**TAGG**
GCTTTTTTACCATCAAAATTTTTTAAAGTGCTAATGTGTATTGCAACCAATGGTAGTCTTAA
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATG
TAGGAAGATATTAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTTAT
TTAA

FIGURE 62

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGVWNQFFVPEEMNTTSHH
IGQLRSDLNNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSNDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTGIVIRISSKMDRELQDEYVWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHFHYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGS LAGSLSSLES AVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN
```

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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FIGURE 63

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGC
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGTGCAGGCTTGAC
AAGTCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACCTTACCCTTGAAGAAGTGCTGTTC
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTG
GATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAA
TAACTAACCCCCTTTCCTTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC
CAAAGGAAGATGGGAAGCCAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA
TAGATATTTATTGATAACATTTTCATTGTAACCTGGTGTTCATACACAGAAAACAATTTATTT
TTTAAATAATTGTCCTTTTCCATAAAAAAGATTACTTTCCATTCTTTAGGGGAAAAAACCC
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA
TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

64/75

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185

><subunit 1 of 1, 179 aa, 1 stop

><MW: 20011, pI: 8.10, NX(S/T): 3

MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

65/75

FIGURE 65

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCTCCGGCTGCGAGAAAGGA
CGCGCGCCCTGCGTCGGGCGAAGAAAAGAAGCAAACTTGTCTGGGAGGGTTTCGTCATCAAC
CTCCTTCCCGCAAACCTAAACCTCCTGCCGGGGCCATCCCTAGACAGAGGAAAGTTCCTGCA
GAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGCTGGCTGTGGAATTAGATCTGT
TTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGCACCGGGTTGG
CGCTGCCCCGAGTGGAACCGACAGTTTGGCAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCG
GTTGTTGTTTCACTGTCGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGG
TCCGAAGAGCGCTGCGCTCCTACTCGCGTTCGCTTCTTCTCCTCTTCTCGGTTCCCTACTGTGA
AATCGCAGCGACATTTACAAAGGCCTCCGGGTCTTACCGAGACCGATCCGCAGCGTTTGGCC
CGGTCGTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGAAATGGCGAGGTTCCCGAAGGC
CGACCTGGCCGCTGCAGGAGTTATGTTACTTTGCCACTTCTTACGGACCAGTTTTCAGTTTCG
CCGATGGGAAACCCGGAGACCAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCCTTCCCT
CACACAGAGGAGGAGGTGGAAGTTGATTACACACGCTACAGCCACAGGTGGAAAAGAACTT
GGACTTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGAGCCCA
GAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGAT
ACAGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTT
ATGGGTGAACATAGACCAATGGAAAAAGATAAAGTGAAGATTCATGGAATATTGTCCAATA
CTCATCGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGGCCACTTCCTA
CGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGTCGTACATCGAATGCT
AACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCCAGTGTATCCAGAAATT
CAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTC
CAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCTGCTCATGGATGGACGAAT
CATCTTTGGATACAAAGAAATTCCTGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAG
TGAAAGTCGGACTGTCCGATGCATTTGTCTGTGCCACAGGATCCAACAAATTCCCAATGTT
CGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAAAATTACCAACAT
TTCGGCTGTGGAGATGACCCCATTAACCCACATGCCTCCAGTTTAAACAGATGTGGCCCCCTGTG
TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGA
TTTGATCGTCATCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGAT
GTGTGAGAATACAGAACCAGTGGAAACTTCTTCTCGAACCACCACAACCGTAGGAGCGACAA
CCACCCAGTTTCAGGGTCCTAACTACCACCAGAAGAGCAGTGACTTCTCAGTTTCCCACCAGC
CTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGCTTCTACAGA
TGACAGTGCAGCTGAGAAGAAAGGGGGAACCTCCACGCTGGCCTCATCATTGGAATCCTCA
TCCTGGTCCCTCATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACA
TCAGCAGCCAGCATCTTCTTTATTGAGAGACGCCCAAGCAGATGGCCTGCGATGAAGTTTAG
AAGAGGCTCTGGACATCCTGCCTATGCTGAAGTTGAACAGTTGGAGAGAAAGAAGGCTTTA
TTGTATCAGAGCAGTGCTTAAATTTCTAGGACAGAACAACACCAGTACTGGTTTACAGGTGT
TAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACACACACACAAACAAGCTC
TAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGG
TAAACAAAAAACTAAACTTATACAAGATACCATTTTACTGAACATAGAATTCCCTAGTGG
AATGTCATCTATAGTTCACTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTA
TAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAGGGATCAGAAAAAAAATCATAATAAAGC
TTTAGTTCATGAGGG

FIGURE 66

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTAQAFPHTEEEVEVD SHAYS
HRWKRNLDFLKAVDTNRASVGQDSPEPRSFTDLLLDDGQDNNTQIEEDTDHNYIISRIYGPS
DSASRDLWVNIDQMEKDKVKI HGILSNTHRQAARVNLSFDFFYGHFLREITVATGGFIYTG
EVVHRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQAT
LLMDGRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQ
MSKITNISAVEMTLPPTCLQFNRCGPCVSSQIGFNC SWCSKLQRCSSGFDRHRQDWVDSGCP
EESKEKMCENTEPVETSSRTTTTVGATTTQFRVLTTTRRAVTSQFPTSLPTEDDTKIALHLK
DNGASTDDSAAEKKGGLHAGLIIGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

FIGURE 67A

GCAGCCCTAGCAGGGATGGACATGATGCTGTTGGTGCAGGGTGCTTGTGCTCGAACCAGTG
GCTGGCGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCCTCCTGCCTCCCGGCTGGACAGA
GTGTGGACTTCCCCTGGGCGGCCGTGGACAACATGATGGTCAGAAAAGGGACACGGCGGTG
CTTAGGTGTTATTTGGAAGATGGAGCTTCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTAT
TTTTGCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAA
GGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACAGTGTCT
GTTCAGACTCAACATACACCCAGAACAATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAA
GATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCACTCTTACTTGTT
TGGCCACTGGGAAACCAGAGCCTTCCATTTCTTGGCGACACATCTCCCCATCAGCAAAACCA
TTTGAAAATGGACAATATTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAATATGA
ATGCAGTGCAGAAAATGATGTGTCATTCCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACT
TTGCTCCTACTATTTCAGGAAATTAAATCTGGCACCGTGACCCCCGGACGCAGTGGCCTGATA
AGATGTGAAGGTGCAGGTGTGCCGCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCT
CTTCAATGGCCAACAAGGAATTATTATTCAAAATTTTAGCACAAGATCCATTCTCACTGTTA
CCAACGTGACACAGGAGCACTTCGGCAATTATACTTGTGTGGCTGCCAACAAGCTAGGCACA
ACCAATGCGAGCCTGCCTCTTAACCCTCCAAGTACAGCCCAGTATGGAATTACCGGGAGCGC
TGATGTTCTTTTCTCCTGCTGGTACCTTGTGTTGACACTGTCCTCTTTCACCAGCATATTCT
ACCTGAAGAATGCCATTCTACAATAAATTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCT
GAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTAAAAGCAGCGTGGGATATAATC
AGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATTATGTAAATACTTTAAT
TCTACTCTTTTTTGTATTAGCTACATTACCTTGTGAAGCAGTACACATTGTCCTTTTTTTAAG
ACGTGAAAGCTCTGAAATTACTTTTAGAGGATATTAATTGTGATTTTCATGTTTGTAATCTAC
AACTTTTCAAAGCATTCAGTCATGGTCTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAA
TATTGCAGTGAATATGTGATTCTTTAAGGCTGCAATACAAGCATTTCAGTTCCTGTTCAT
AAGAGTCAATCCACATTTACAAAGATGCATTTTTTTTCTTTTTTGATAAAAAAGCAAATAATA
TTGCCCTTCAGATTATTTCTTCAAATATAACACATATCTAGATTTTTCTGCTCGCATGATAT
TCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCAGCTCTGCTTCTCTTCTCTGT
AAGTTCAGCATGGGTGTGCCTTCATACAATAATATTTTTCTCTTTGTCTCCAACATAATAA
AATGTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACCAGAGTGATCAAGTTAAACCA
TACACTATCTCTAAGTAACGAAGGAGCTATTGGACTGTAAAAATCTCTTCTGCACTGACAA
TGGGGTTTGAGAATTTTGCCCCACACTAACTCAGTTCTTGTGATGAGAGACAATTTAATAAC
AGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGA
AATCATTCCCTTTAAATGACAGCACAGTCCACTCAAAGGATTGCCAGCAATACAGCATCT
TTTCCTTTCAGTAGTCCAAGCCAAAAATTTAAGATGATTTGTCAGAAAGGGCACAAAGTCC
TATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTATTTTATTTTGTGGCAGCTAA
GTTAGTATGACAGAGGCAGTGCTCCTGTGGACAGGAGCATTTTGCATATTTTCCATCTGAAA
GTATCACTCAGTTGATAGTCTGGAATGCATGTTATATATTTTAAACTTCCAAAATATATTA
TAACAAACATTCTATATCGGTATGTAGCAGACCAATCTCTAAAATAGCTAATTCTTCAATAA
AATCTTTCTATATAGCCATTTTCAGTGCAACAAGTAAAATCAAAAAAGACCATCCTTTATTT
TTCCTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACACCAGTGATGAGAATAT
CTTAAGATAAGTAATTATCAAATTATTGTGAATGTTAAATTATTTCTACTATAAAGAAGCAA
AACTACATTTTTGAAGGAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGATGG
TTTCACTCTTTACTAAAGAAAGGCCATCACCTTGAAAGCCATTTTACAGGTTTGATGAAGTT
ACCAATTTTCAGTACACCTAAATTTCTACAAATAGTCCCCTTTTACAAGTTGTAACAACAAG
ACCCTATAATAAAATTAGATACAAGAAATTTTGCAGTGGTTATACATATTTGAGATATCTAG
TATGTTGCCCTAGCAGGGATGGCTTAAAAACTGTGATTTTTTTTCTTCAAGTAAAACCTTAGT
CCCAAAGTACATCATAAATCAATTTTAATTAGAAAAATGAATCTTAAATGAGGGGACATAAG
TATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAACTGTAAT
AAATGTATGACATTATTTTGATTGATACATTAAAAAAGAGTTTTTGAACAAATATGGCATT
TAACTTTATTATTTATTTGCTTTTAAAGAAATATCTTTGTGGAATTGTTGAATAAACTATAA
AATATTATTTGTATTGCAGCTTTAAAGTGGCACACTCCATAATAATCTACTTACTAGAAAT

FIGURE 67B

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC
AAGAATGCATATTATTCAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT
TGTAGGTAAATTGAGGTATAAACTATGGATGAACCAATAATTAGTTCAAAGTGTTGTCATG
ATTCCAAATTTGTGGAGTCTGGTGTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT
CAGTAGCTATATGTATTTGCCCTTTATGTTAGAAGAGACTTTCCTTGAGTGACATTTTTAAATA
GAGGAGGTATTCACTATGTTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA
CAGAGTGAAATCATGAGTATTTATGAGTTCAATATTGTCAAATAAGGCTACAGTATTTGCTT
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA
AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTTTCAGAATAG
CAGTTTTATAAATTGATTTATCTTTTAATCTATAACAATTTGTGTTAGCTGTTTCATTTCAGG
ANTATATTTTCTACAAGTTCCACTTGTGGGACTCCTTTTGTGCCCCCTATTTTTTTTTTAAAG
AAGGAAGAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAGAAAAAGAATG
AAAAGGAAAGGCAGTAAAGAGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGAAGGAAGAATCAGAGTATTAGG
GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAAGTATGTTTTTCAA
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAAGTTCCTATTATGCAGCAATTATAT
AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTGGAGACACTAAAAGATTTGAG
AGGGAGAATTTCAAACCTTAAAGCCACTTTTGGGGGGTTTATAACTTAACTGAAAAATTAATG
CTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGAGAACTGAGAAAATTACCCAG
GTAATTCAGGGAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA
ACTCTGAAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA
GATTCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA
CATCCATATTTCATAACCTGATGTAAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC
TCAGTTTATCAATTAAAAA

FIGURE 68

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259
><subunit 1 of 1, 354 aa, 1 stop
><MW: 38719, pI: 6.12, NX(S/T): 6
MDMMLLVQGACCSNQWLA AVL LSLCCLLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYL
EDGASKGAWLNRSSII FAGGDKWSV DPRVSISTLNKR DYSLQIQNV DVTDDGPYTCSVQTQH
TPRTMQVHLTVQVPPKIYDISNDMTVNEG TNVTLTCLATGKPEPSISWRHISPSAKPFENGQ
YLDIYGITRDQAGEYEC SAENDVSFPDVRKVKVVVNFAPT IQEIKSGTVTPGRSGLIRCEGA
GVPPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQE HFGNYTCVAANKLGT TNASL
PLNPPSTAQYGITGSADVLFSCWYLVLT LSSFTSIFYLKNAILQ
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 322-343

N-glycosylation sites.

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

Tyrosine kinase phosphorylation site.

amino acids 180-188

N-myristoylation sites.

amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,
304-310, 321-327

Myelin P0 protein.

amino acids 94-123

FIGURE 69

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACA
ATTTACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTG
TTCTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCA
AGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT
TTAATTAAGGGGTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCT
GCGTCACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAAA
CAGCTGGAGATTGGGCTTAAATACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAA
CATTGATTTTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA
GCCCACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCAC
CGCTGCCCTGCCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGACCTCCCAG
GCCAGTGCCGGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGC
ACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCT
TCTCCTCCTGCAAATAG

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FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175

><subunit 1 of 1, 155 aa, 1 stop

><MW: 17194, pI: 10.44, NX(S/T): 0

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLL
SGATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK

Important features of the protein:

Transmembrane domain:

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCC**ATG**GCGTGGAGCCTTGGGA
GCTGGCTGGGTGGCTGCCTGCTGGTGTGTCAGCATTGGGAATGGTACCACCTCCCGAAAATGTC
AGAATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGG
GAACCTGACTTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATA
CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC
AGGGCTGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGA
CACCATTATTGGACCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTT
TCTTAGCCCCCTAAAATTGAGAATGAATACGAAACTTGGACTATGAAGAATGTGTATAACTCA
TGGACTTATAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCA
GTATGACTTTGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTTCAAGTTCGAG
GGTTTCTTCCTGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACC
CATGACGAAACGGTCCCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGT
CTGCCTGGCACTCCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACG
CCTTCTCCCCCTAGGAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT
AACACACTTCTGTTTTTCTCCTTTCCATTGTGCGGATGAGAATGATGTTTTTGACAAGCTAAG
TGTCATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA
CCCCGCTGGGCAGGGGCCCCAAAGC**TAG**GCTCTGAGAAGGAAACACACTCGGCTGGGCACA
GTGACGTACTCCATCTCACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGA
CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT
TTTAAAGGCTGTCTTGGCAAAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCA
TGATGTTTTTCAGAAGTTGGCCACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAA
GATCATGTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCA
CCTTAGAGGTCGAGGCAGGCGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAATA
TGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTAT
AATCCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA
GGTTGCAGTGAGCCGAGATAGCGGCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCAT
CTCAAAAAAAAAAAAAAAAAAATTGTGAGAAACAGAAATACTTAAATGAGGAATAAGAATGG
AGATGTTACATCTGGTAGATGTAACATTCTACCAGATTATGGATGGACTGATCTGAAAATCG
ACCTCAACTCAAGGGTGGTCAGCTCAATGCTACACAGAGCACGGACTTTTGGATTCTTTGCA
GTACTTTGAATTTATTTTTCTACCTATATATGTTTTATATGCTGCTGGTGTCTCCATTAAAGT
TTTACTCTGTGTTGC

73/75

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551

><subunit 1 of 1, 325 aa, 1 stop

><MW: 37011, pI: 5.09, NX(S/T): 4

MAWSLGSWLGGLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSDWVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTT
YCVQVRGFLPDRNKAGEWSEPVCETTHDETVPSSWMAVILMASVFMVCLALLGCFSLWCV
YKKTKYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNP
DSCSLGTPPGQGPQS

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

FIGURE 73

CGAGCGCCAACCCGCTAGCGCCTGAATCCGGCGTGCTGCCCGCTCGCCGCCCGCC**ATG**GCCC
GCGCAGCCCCGCTGCTCGCCGCGTTGACCGCGCTCCTCGCCGCCCGCGCTGCTGGCGGAGAT
GCCCCGCCGGGCAAAATCGCGGTGGTTGGGGCTGGGATTGGGGGCTCTGCTGTGGCCCATTT
TCTCCAGCAGCACTTTGGACCTCGGGTGCAGATCGACGTGTACGAGAAGGGAACCGTGGGTG
GCCGCTTGGCCACCATCTCAGTCAACAAGCAGCACTATGAGAGCGGGGCTGCCTCCTTCCAC
TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGGCTGAGGCACCGGCGCGAGGT
GGTGGGCAGGAGCGCCATCTTCGGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACC
TGCTGAACCTCTTCCGCCTCTGGTGGCACTATGGCATCAGCTTCCTGAGGCTGCAGATGTGG
GTGGAGGAGGTGATGGAGAAGTTCATGAGGATCTATAAGTACCAGGCCACGGCTATGCCTT
CTCGGGTGTGGAGGAGCTGCTCTACTCACTGGGGGAGTCCACCTTTGTAAACATGACCCAGC
ACTCTGTGGCTGAGTCCCTGCTGCAGGTGGGCGTCACGCAGCGCTTTATTGATGATGTCGTT
TCTGCTGTCTGCGGGCCAGCTATGGCCAGTCAGCAGCGATGCCCGCCTTTGCAGGAGCCAT
GTCACTAGCCGGGGCCCCAAGGCAGCCTGTGGTCTGTGGAAGGAGGCAATAAGCTGGTTTGT
CCGGTTTGTGAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTGACCTCTGTGACCCTG
CACAGCACAGAGGGGAAAGCCCTGTACCAGGTGGCGTATGAGAATGAGGTAGGCAACAGCTC
TGACTTCTATGACATCGTGGTCATCGCCACCCCCCTGCACCTGGACAACAGCAGCAGCACT
TAACCTTTGCAGGCTTCCACCCGCCATTGATGACGTGCAGGGCTCTTTCCAGCCCACCGTC
GTCTCCTTGGTCCACGGCTACCTCAACTCGTCCTACTTCGGTTTCCAGACCCTAAGCTTTT
CCCCTTTGCCAACATCCTTACCACAGATTTCCCCAGCTTCTTCTGCACTCTGGACAACATCT
GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCCAGGAGGCAGCTGTTTGGCGA
GTCCAGTCCCCCAAGCCCCCTCTTTCGGACCCAGCTAAAGACCCTGTTCGGTTCCTATTACTC
AGTGCAGACAGCTGAGTGGCAGGCCCATCCCCTCTATGGCTCCCGCCCCACGCTCCCGAGGT
TTGCACTCCATGACCAGCTCTTCTACCTCAATGCCCTGGAGTGGGCGGCCAGCTCCGTGGAG
GTGATGGCCGTGGCTGCCAAGAATGTGGCCTTGCTGGCTTACAACCGCTGGTACCAGGACCT
AGACAAGATTGATCAAAAAGATTTGATGCACAAGGTCAAGACTGAACTGTGAGGGCTCTAGG
GAGAGCCTGGGAACTTTCATCCCCCACTGAAGATGGATCATCCCACAGCAGCCCAGGACTGA
ATAAGCCATGCTCGCCCCACCAGGCTTCTTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG
ACCTACTGTCTGCCTATATTAAGGGTCCACACGGCGGGCTGCTGCTTTTTTTTTTAAGGGGAAA
GTAAGAAAAGAGAAGGAAATCCAAGCCAGTATATTTGTTTTATTTATTTTTTTAAGAAGAA
AAAAGTTCATCTTCACAAGGTGCTTCAGACTTGGTTTTCTTAGCTAGAAACCAGAAGACTACG
GGAGGGAATATAAGGCAGAGAACTATGAGTCTTATTTTATTACTGTTTTTCACTACCTACTC
CCACAATGGACAATCAATTGAGGCAACCTACAAGAAAACATTTACAACCAGATGGTTACAAA
TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGCTCCTGGTTACTGTGGACT
TGATGGATTTGAAGTACCTAGTTCAGAACTCCCTAGTCACCATCTCCAAGCCTGTCAACATC
ACTGCATATTGGAGGAGATGACTGTGGTAGGACCCAAGGAAGAGATGTGTGCCTGAATAGTC
GTCACCATATCTCCAAGCTTCCTGGCAACCAGTGGGAAAAGAAACATGCGAGGCTGTAGGAA
GAGGGAAGCTCTTCCTTGGCACCTAGAGGAATTAGCCATTCTCTTCCTTATGCAAAGATTGA
GGAATGCAACAATATAAAGAAGAGAAGTCCCCAGATGGTAGAGAGCAGTCATATCTTACCCC
TAGATGTTTCATCCCAGCAGAAGAAAGAAGAGGTGTTGGGGTAGGATTCTTCAGAGGTTAGC
CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTTCTTTGCTTT
TTCTACAAACCCTTAAAAATCACTTGTTTAAAAAAGAAAGTAAAGCCCTTTTCATTCAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 74

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510
><subunit 1 of 1, 494 aa, 1 stop
><MW: 54646, pI: 7.27, NX(S/T): 6
MARAAPLLAALTALLAAAAAGGDAPPGKIAVVGAGIGGSAVAHFLQQHFGPRVQIDVYEKGT
VGGRLATISVVKQHYESGAASFHSLSLHMQDFVKLLGLRHRREVVGSAIFGGEHFMLEETD
WYLLNLFRLWWHYGISFLRLQMWVEEVMEKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM
TQHSVAESLLQVGVTQRFIDDVVSAVLRASYGQSAAMPFAFAGAMSLAGAQQSLWSVEGGNKL
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS
SNLTFAGFHPPIDDVQGSFQPTVVSLVHGYNSSYFGFPDPKLFPPFANILTTDFPSFFCTLD
NICPVNISASFRRKQPQEAQVWRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPYGSRPTL
PRFALHDQLFYLNLEWAASSVEVMAVAANKVALLAYNRWYQDLKIDQKDLMHKVKTEL
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Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

N-myristoylation sites.

amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,
237-243, 429-435